

FIG. 1

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CDNA: 1 - 8117 [SEQ ID NO:1] CDS: 170 - 7876 [SEQ ID NO:2] AA: [SEQ ID NO:3]

cacccggggagacgtcttagacagtcgtggttcctgtgatctgtgtcctctt											
tgcagaagttctgtgtccatctcatgtgctgcgtgtgtctgtaaagcctcat											
tccgtgctgtctggcaggaagctccatctcatctcatct											
M A I S S R L A L gcactgcctcagc ATG GCC ATC TCA TCA CGC CTC GCC CTG											
W E Q K I R E E D K S P P TGG GAG CAG AAG ATT CGG GAA GAG GAC AAG AGC CCT CCA	22 235										
P S S P P P L F S V I P G CCA TCC TCG CCC CCT CCT TTC TCT GTC ATC CCA GGG	35 274										
G F I K Q L V R G T E K E GGC TTC ATT AAG CAA CTG GTC CGG GGG ACT GAA AAA GAG	48 313										
A K E A R Q R K Q L A V A GCC AAG GAA GCG AGA CAG AGG AAG CAG TTA GCT GTC GCC	61 352										
S P E R E I P E I S I S Q TCT CCA GAA CGA GAG ATC CCA GAA ATT TCC ATC AGC CAA	74 391										
P N S K S S S G T R S G S CCC AAC AGC AAG TCC AGC AGT GGC ACC AGA TCT GGA AGC	87 430										
Q Q I S Q D D Q S S S P G CAG CAG ATC TCT CAG GAC GAC CAG TCA AGC TCT CCT GGG	100 469										
S S D I L G K E S E G S R AGC TCA GAC ATT CTG GGC AAG GAG AGC GAG GGG TCC CGC	113 508										
S P D P E Q M T S I N G E AGC CCC GAC CCT GAG CAG ATG ACA AGC ATC AAT GGT GAG	126 547										
K A Q E L G S S A T P T K AAG GCC CAG GAG CTG GGC TCC AGT GCG ACA CCA ACC AAA	139 586										
K T V P F K R G V R R G D AAG ACT GTC CCC TTC AAG AGG GGC GTG AGG AGG GGT GAT	152 625										
V L L M V A K L D P D S A GTG TTG TTG ATG GTG GCC AAG CTG GAC CCG GAC TCA GCC	165 664										
K P E K T H P H D A P P C	178										

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AAG	CCA	GAG	AAG	ACT	CAT	CCC	CAT	GAC	GCC	CCC	CCT	TGC	703
K AAG	T ACC	S TCT	P CCC	P	A GCC	T ACA	D GAT	T ACT	G GGA	K AAG	E GAA	K AAG	191 742
K	G	E	T	S	R	T	P	C	G	S	Q	A	204
AAA	GGG	GAG	ACC	TCT	AGG	ACT	CCT	TGT	GGC	TCC	CAG	GCC	781
S	T	E	I	L	A	P	K	A	E	K	T	R	217
AGC	ACC	GAG	ATC	TTG	GCC	CCG	AAA	GCT	GAG	AAG	ACC	CGG	820
T ACT	.GGG	G GGT	$_{\mathtt{CTT}}^{\mathtt{L}}$	G GGG	D GAC	P CCA	G GGC	Q CAA	G GGA	T ACT	V GTG	A GCA	230 859
L	K	K	G	E	E	G	Q	S	I	V	G	K	243
CTG	AAA	AAA	GGC	GAG	GAG	GGT	CAA	AGC	ATA	GTG	GGG	AAG	898
G	L	G	T	P	K	T	T	E	L	K	E	A	256
GGG	CTT	GGG	ACC	CCC	AAG	ACC	ACA	GAG	CTG	AAA	GAG	GCT	937
E GAG	P	Q CAG	G GGC	K AAA	D GAC	R AGG	Q CAG	G GGG	T ACC	R AGG	P CCC	Q CAA	269 976
A GCC	Q CAA	G GGG	P	G GGC	E GAG	G GGG	V GTG	R CGA	P CCA	G GGG	K AAA	A GCA	282 1015
E	K	E	G	A	E	P	T	N	T	V	E	K	295
GAG	AAG	GAG	GGA	GCA	GAG	CCC	ACA	AAC	ACG	GTG	GAA	AAG	1054
G	N	V	S	K	D	V	G	S	E	G	K	H	308
GGG	AAT	GTC	TCT	AAG	GAC	GTA	GGG	AGT	GAA	GGG	AAG	CAC	1093
V GTA	R AGG	P	Q CAA	I ATC	P CCT	G GGG	R AGA	K AAG	W TGG	G GGA	G GGT	F TTC	321 1132
L	G	R	R	S	K	W	D	G	P	Q	N	K	334
CTG	GGA	AGA	AGG	AGT	AAG	TGG	GAC	GGT	CCC	CAG	AAT	AAG	1171
K	D	K	E	G	V	L	L	S	K	A	E	K	347
AAG	GAC	AAA	GAA	GGG	GTG	CTC	TTA	AGT	AAG	GCA	GAG	AAG	1210
T	G	E	P	Q	T	Q	M	E	K	T	S	Q	360
ACA	GGT	GAG	CCT	CAG	ACC	CAG	ATG	GAG	AAG	ACA	AGC	CAA	1249
V	Q	G	E	L	G	D	D	L	R	M	G	E	373
GTG	CAG	GGC	GAG	TTG	GGG	GAC	GAT	CTG	AGA	ATG	GGG	GAG	1288
K	A	G	E	L	R	S	T	T	G	K	A	G	386
AAA	GCA	GGT	GAG	CTT	CGG	AGC	ACG	ACT	GGG	AAG	GCA	GGT	1327
E GAG	S	W TGG	D GAT	K 'AAG	K AAG	E GAA	K AAG	M ATG	G GGG	Q CAA	P CCC	Q CAG	399 1366

FIG. 2B

G K S G N A G E A R S Q T 412 GGT AAG TCC GGG AAC GCA GGT GAA GCT CGG AGT CAG ACA 1405 E K G C E A P K E V S T M GAG AAG GGC TGT GAA GCC CCA AAG GAG GTG AGC ACA ATG 1444 V E S P A A P G K G G W P GTG GAG TCG CCA GCA GCT CCT GGG AAG GGA GGC TGG CCA 438 451 G S R G Q E A E E P C S R GGA AGC CGT GGG CAG GAA GCA GAG GAG CCC TGC TCA AGA A G D G A G A L E T E L E GCA GGT GAT GGG GCT GGT GCC CTG GAG ACA GAG CTG GAA 1561 G P S Q P A L E K D A E R GGA CCC AGC CAG CCT GCT CTG GAG AAG GAT GCA GAA AGG 477 P R I R K E N Q D G P A P CCT CGG ATA CGG AAG GAG AAC CAA GAC GGG CCA GCC CCG 490 1639 503 516 Q A P E D R W Y E A E K V CAG GCT CCT GAG GAC AGA TGG TAT GAG GCA GAG AAA GTC W L A Q K D G F T L A T V TGG CTG GCT CAG AAG GAT GGA TTT ACT CTT GCT ACG GTG 529 542 L K P D E G T A D L P A G CTA AAG CCA GAT GAG GGA ACA GCA GAC CTG CCA GCA GGA 1795 1834 E V D E E H V H R A N P P GAG GTG GAT GAG GAG CAT GTC CAT CGG GCC AAC CCT CCT 1912 V N E S S V L N T L L Q R GTC AAC GAA TCC AGT GTC CTG AAC ACG CTT CTG CAG CGC 594 1951 Y K A Q L L H T C T G P D TAC AAA GCT CAG CTG CAC ACC TGC ACA GGG CCT GAT 607 1990 L I V L Q P R G P S V P S CTG ATT GTC CTC CAG CCC CGG GGG CCC TCG GTG CCT TCT

FIG. 2C

A G K V P K G R R D G L P GCA GGG AAG GTG CCC AAG GGC CGC CGG GAT GGC CTG CCT A H I G S M A Q R A Y W A GCC CAC ATT GGC TCC ATG GCA CAG CGG GCA TAC TGG GCG L L N Q R R D Q S I V A L CTG CTG AAC CAG CGG AGA GAC CAG AGC ATT GTG GCC CTG  ${\tt G}$  R S G A G K T T C C E Q GGC CGG AGT GGC GCT GGG AAG ACC ACC TGC TGT GAG CAG V L E H L V G M A G S V D GTC CTG GAA CAC CTG GTG GGG ATG GCA GGC AGT GTG GAT 685 2224 698 G R V S V E K I R A T F T GGC AGG GTC TCA GTG GAG AAG ATC CGA GCC ACC TTC ACT V L R A F G S V S M A H S GTC CTC CGG GCC TTC GGC TCT GTG TCC ATG GCC CAC AGC 711 2302 724 R S A T R F S M V M S L D CGC AGT GCC ACC CGG TTC TCC ATG GTG ATG TCG CTG GAC F N A T G R I T A A Q L Q TTC AAC GCT ACA GGC CGC ATC ACA GCT GCT CAG CTC CAG T M L L E K S R V A R Q P ACA ATG CTT TTG GAG AAG AGC CGC GTG GCA CGG CAG CCG 750 E G E S N F L V F S Q M L GAA GGG GAA AGT AAC TTC CTG GTT TTC TCC CAG ATG CTG A G L D L D L R T E L N L GCT GGA TTG GAC TTG GAT CTC AGG ACG GAG CTG AAC CTG 776 2497 H Q M A D S S S F G M G V CAC CAG ATG GCA GAT AGC AGC TCC TTT GGC ATG GGC GTG 789 W S K P E D K Q K A A A A TGG TCC AAG CCT GAA GAT AAA CAG AAG GCG GCA GCT GCC 815 828 S E S E Q R A V W R V L A TCA GAG AGC GAG CAG CGG GCT GTT TGG CGG GTC CTG GCA 2653 841 A I Y H L G A A G A C K V GCC ATC TAC CAC CTG GGC GCG GCG GCC TGC AAA GTG 2692 Y 854 R F E W Α G R K

FIG. 2D

GGT CGG AAG CAG TTC ATG AGG TTT GAG TGG GCA AAC TAC A A E A L G C E Y E E L N GCA GCT GAG GCC CTG GGC TGC GAG TAT GAG GAG CTG AAC T A T F K H H L R Q I I Q ACG GCC ACC TTC AAG CAC CTT CGA CAG ATC ATC CAG Q M T F G P S R W G L E D CAA ATG ACG TTT GGG CCA AGC CGA TGG GGC CTC GAG GAT E E T S S G L K M T G V D GAG GAA ACC AGC TCA GGG CTC AAG ATG ACA GGA GTG GAC C V E G M A S G L Y Q E L TGT GTG GAG GGG ATG GCC TCG GGC CTG TAC CAG GAA CTC S P G F Q N P R H Q G K D TCT CCA GGC TTC CAG AAC CCC CGG CAC CAG GGC AAG GAC R A A T F E E L C H N Y A CGG GCG GCC ACC TTT GAG GAG CTG TGC CAC AAC TAC GCC H E R L Q L L F Y Q R T F CAT GAG CGC CTG CAG CTG CTG TTC TAC CAG CGG ACC TTT V S T L Q R Y Q E E G V P GTC TCC ACG CTA CAG CGA TAT CAA GAG GAA GGT GTT CCT V Q F D L P D P S P G T T GTG CAG TTT GAC CTC CCG GAC CCC TCC CCA GGG ACC ACC V A V V D Q N P S Q Q V R GTG GCT GTT GTG GAT CAA AAT CCC TCT CAG CAG GTC CGC L P A G G G A Q D A R G L TTA CCA GCT GGA GGA GGT GCC CAG GAT GCC AGA GGC CTT TTC TGG GTC TTA GAT GAG GAA GTC CAT GTA GAG GGC TCC S D S V V L E R L C A T F AGT GAC AGT GTG GTG CTC GAG CGT CTG TGT GCT ACT TTC E K K G A G T E G S S A L GAG AAA GGA GCT GGG ACT GAA GGG TCC TCT GCC CTG

FIG. 2E

R T C E Q P L Q C E I F H CGG ACC TGT GAG CAG CCC CTC CAG TGT GAG ATT TTC CAC Q L G W D P V R Y D L T G CAG TTG GGA TGG GAC CCT GTG CGG TAC GAC CTC ACG GGC W L H R A K P N L S A L D TGG CTC CAC AGA GCC AAG CCC AAC CTC TCG GCC CTG GAT 1114 3511 A P Q V L Q Q S K R E E L GCA CCC CAG GTC CTG CAA CAG TCA AAA AGA GAG GAG CTG 1127 R S L F Q A R A K L P P V CGG AGT CTA TTC CAG GCC CGG GCC AAG CTG CCT CCT GTG 1140 3589 1153 C R A V A G L E G T S Q Q TGC CGG GCT GTG GCA GGC CTG GAG GGC ACC TCC CAG CAG 1166 A L Q R S R M V R R T F A GCC CTG CAG AGG AGC CGC ATG GTG AGG AGG ACC TTT GCC 3667 S S L A A V R R K A P C S AGC AGC CTT GCC GCG GTG AGG AGG AAA GCC CCG TGC TCC 1179 3706 1192 Q I K L Q M D A L T S M I CAG ATC AAG CTG CAG ATG GAT GCG CTG ACC AGC ATG ATC 3745 K R S R L H F I H C L V P AAA AGG TCC CGG CTG CAC TTT ATC CAC TGC CTG GTA CCA 1205 1218 N P V V E S R S G Q E S P AAC CCT GTG GTG GAA AGC AGG AGT GGG CAG GAA TCT CCA 3823 P P P Q P G R D K P G A G CCA CCA CCG CAG CCT GGT AGA GAC AAG CCT GGG GCA GGT 1231 3862  $\tt G$   $\tt P$   $\tt L$   $\tt A$   $\tt L$   $\tt D$   $\tt I$   $\tt P$   $\tt A$   $\tt L$   $\tt R$   $\tt V$   $\tt Q$   $\tt GGA$  CCT CTG GCC CTG GAT ATC CCA GCA CTG AGG GTC CAG 1244 1257 L A G F H I L E A L R L H CTT GCT GGG TTC CAC ATC CTG GAG GCT CTG CGT CTG CAT 3940 R T G Y A D H M G L T R F AGG ACA GGC TAT GCT GAC CAC ATG GGG CTC ACT CGC TTC 1270 1283 R R Q F Q V L D A P L L K CGC CGG CAA TTC CAG GTG CTG GAC GCT CCA CTC CTG AAG 4018 AAG CTC ATG TCG ACC TCC GAG GGA ATA GAT GAA AGG AAG

FIG. 2F

A V E E L L E T L D L E K GCC GTG GAG GAG CTC CTG GAG ACC CTG GAT CTG GAA AAG K A V A V G H S Q V F L K AAG GCG GTG GCT GTG GGG CAC AGC CAA GTT TTT CTC AAG 1322 4135 A G V I S R L E K Q R E K GCA GGT GTG ATC TCC AGG CTT GAG AAG CAG CGA GAG AAG 1335 4174 L V S Q S I V L F Q A A C CTG GTA TCT CAG AGC ATC GTT CTC TTC CAG GCG GCT TGC 1348 4213 K G F L S R Q E F K K L K AAG GGC TTT CTG TCT CGC CAG GAA TTC AAG AAG CTG AAG 1361 4252 I R R L A A Q C I Q K N V ATT CGC CGA CTG GCT GCA CAG TGC ATC CAG AAG AAT GTG 1374 4291 1387 A V F L A V K D W P W W Q GCT GTG TTC CTC GCA GTC AAG GAC TGG CCA TGG TGG CAG 4330 1400 4369 G T E Q L R A K E E E L T GGA ACT GAG CAG CTC CGA GCC AAG GAG GAG GAG CTT ACA 1413 4408 T L R R K L E K S E K L R ACG CTA AGA CGG AAG CTA GAA AAA TCA GAG AAG TTG CGG 1426 1439 N E L R Q N T D L L E S K AAT GAA CTC CGG CAG AAC ACA GAT CTG CTA GAA AGC AAG 4486 I A D L T S D L A D E R F ATT GCT GAC TTG ACC TCT GAC CTT GCC GAT GAG CGC TTC 4525 1465 K G D V A C Q V L E S E R AAA GGT GAT GTG GCC TGC CAG GTG CTG GAG AGT GAG CGG 4564 A E R L Q A F R E V Q E L GCA GAG CGG CTA CAG GCC TTC CGG GAG GTC CAG GAG CTC 1478 4603 K S K H E Q V Q K K L G D AAG AGC AAG CAT GAA CAA GTC CAG AAA AAA CTG GGA GAT 1491 4642 V N K Q L E E A Q Q K I Q GTG AAT AAA CAG TTG GAA GAA GCC CAG CAG AAA ATT CAG 1504 4681 1517 TTG AAT GAC TTG GAA AGG GAT CCC ACT GGA GGA GCA GAC 4720 C 1530 D Α Q Ė Ν R Μ E 0 Μ

FIG. 2G

GAG TGG CAG ATG CGC TTC GAC TGT GCT CAG ATG GAG AAC E F L R K R L Q Q C E E R GAG TTC CTC AGA AAG CGT CTG CAG CAA TGC GAG GAG AGG 1543 4798 L D S E L T A R K E L E Q CTG GAC TCG GAG CTG ACA GCC AGG AAA GAG CTG GAG CAA 1556 4837 K L G E L Q S A Y D G A K AAG CTT GGG GAG TTG CAA AGT GCT TAT GAC GGG GCC AAG 1569 4876 K M A H Q L K R K C H H L AAG ATG GCT CAC CAA CTG AAG AGG AAG TGC CAC CAT CTT 1582 4915 T C D L E D T C V L L E N ACC TGT GAC CTT GAG GAT ACC TGC GTC CTG CTA GAG AAC 1595 4954 Q Q S R N H E L E K K Q K CAA CAA AGT CGA AAC CAT GAG CTG GAG AAG AAG CAG AAG 1608 4993 K F D L Q L A Q A L G E S AAG TTT GAC CTG CAG CTG GCC CAG GCC CTA GGT GAG TCA 1621 5032 V F E K G L R E K V T Q E GTG TTT GAG AAG GGT CTC CGT GAG AAA GTG ACC CAG GAG 1634 5071 1647 N T S V R W E L G Q L Q Q AAC ACC AGT GTC CGG TGG GAG CTA GGC CAG CTT CAG CAG Q L K Q K E Q E A S Q L K CAG CTG AAG CAA AAG GAG CAG GAA GCC TCA CAG CTG AAG 1660 5149 Q Q V E M L Q D H K R E L CAG CAG GTG GAG ATG CTA CAG GAC CAT AAA CGG GAG CTG 1673 5188 L G S P S L G E N C V A G CTG GGG TCA CCC TCT CTG GGG GAA AAT TGC GTT GCT GGC 1686 5227 L K E R L W K L E S S A L TTG AAG GAG AGG CTC TGG AAG TTG GAA TCC AGC GCC CTT 1699 1712 E Q Q K I Q S Q Q E N T I GAG CAA CAG AAA ATC CAG AGC CAG CAG GAA AAC ACC ATC K Q L E Q L R Q R F E L E AAG CAG CTG GAG CTC CGC CAG CGG TTT GAG CTG GAG 1725 5344 I E R M K Q M H Q K D R E ATC GAG CGG ATG AAG CAG ATG CAC CAG AAG GAC CGT GAG 1738 5383 D Q E E E L E D V R Q S C GAC CAG GAG GAA CTG GAG GAT GTC CGT CAG TCC TGC

FIG. 2H

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Q K R L H Q L E M Q L E Q CAG AAG CGG CTT CAT CAG CTG GAA ATG CAG CTG GAG CAA E Y E E K Q M V L H E K Q GAG TAT GAA GAG AAG CAG ATG GTC CTC CAT GAG AAG CAA D. L E G L I G T L C D Q I GAT TTG GAA GGC TTG ATC GGA ACC CTC TGT GAC CAG ATT  ${\tt G}$   ${\tt H}$   ${\tt R}$   ${\tt D}$   ${\tt F}$   ${\tt D}$   ${\tt V}$   ${\tt E}$   ${\tt K}$   ${\tt R}$   ${\tt L}$   ${\tt R}$   ${\tt R}$   ${\tt GGC}$  CAT CGG GAC TTT GAT GTG GAG AAG CGA CTT CGG AGA D L R R T H A L L S D V Q GAC CTC AGG AGG ACA CAT GCA CTG TTG TCA GAC GTG CAG L L L G T M E D G K T S V CTC CTT CTG GGC ACC ATG GAG GAT GGC AAG ACA TCA GTC S K E E L E K V H S Q L E AGC AAG GAG GAG CTG GAG AAA GTG CAC AGC CAG CTG GAG Q S E A K C E E A L K T Q CAG AGT GAA GCC AAG TGT GAG GAG GCC TTG AAG ACG CAG K V L T A D L E S M H S E AAG GTG CTC ACA GCG GAC CTG GAG AGC ATG CAC AGC GAG L E N M T R N K S L V D E CTG GAG AAC ATG ACG CGG AAC AAG AGC CTG GTG GAT GAG Q L Y R L Q F E K A D L L CAG CTG TAC AGG CTG CAG TTT GAG AAG GCG GAC CTC CTG K R I D E D Q D D L N E L AAG CGC ATC GAT GAG GAC CAG GAT GAC CTG AAT GAG CTG M Q K H K D L I A Q S A A ATG CAG AAG CAC AAG GAC CTC ATT GCT CAG TCT GCT D I G Q I Q E L Q L Q L E GAC ATT GGG CAG ATC CAA GAA CTG CAG CTG CAG CTG GAG E A K K E K H K L Q E Q L GAA GCC AAG AAG GAG AAG CAC AAG CTA CAA GAA CAA CTG Q V A Q M R I E Y L E Q S CAG GTG GCT CAG ATG CGC ATC GAG TAC CTG GAA CAG TCC T V D R A I V S R Q E A V ACC GTG GAT CGA GCC ATC GTC AGC AGG CAG GAG GCG GTC

I C D L E N K T E F Q K V ATC TGT GAC CTA GAG AAC AAG ACA GAG TTC CAG AAG GTG Q I K R F E V L V I R L R CAG ATT AAG AGA TTT GAG GTC CTG GTG ATC CGG CTT CGG 1998 6163 2011 D S L I K M G E E L S Q A GAC AGC CTG ATC AAG ATG GGG GAG GAG CTT TCA CAG GCG 6202 2024 A T S E S Q Q R E S S Q Y GCC ACC TCC GAG TCC CAG CAG CGG GAG AGC AGC CAG TAC 6241 Y Q R R L E E L K A D M E TAC CAG CGG CGC CTG GAA GAG CTG AAG GCC GAC ATG GAA 2037 6280 E L V Q R E A E A S R R C GAG CTG GTG CAG CGG GAG GCA GAG GCC AGC CGG CGG TGC 2050 6319 M E L E K Y V E E L A A V ATG GAG CTG GAG AAG TAC GTG GAG GAA CTT GCA GCA GTG 2063 6358 R Q T L Q T D L E T S I R AGG CAA ACC CTC CAG ACA GAC CTG GAG ACA TCC ATT CGG 2076 6397 2089 R I A D L Q A A L E E V A CGG ATT GCC GAC CTG CAG GCT GCC TTG GAA GAA GTG GCA 6436 S S D S D T E S V Q T A V TCC AGT GAC AGT GAT ACT GAG AGT GTC CAG ACG GCA GTG 6475 D C G S S G R K E M D N V GAT TGT GGC AGC AGC GGC CGA AAA GAG ATG GAT AAC GTC 2115 6514 S I L S S Q P E G S L Q S TCC ATC CTC AGC TCC CAG CCA GAG GGC AGC CTG CAG TCC 2128 2141 6592 R T P S R Q S A T S S R I AGG ACT CCT TCT CGA CAG TCA GCC ACC AGC AGC CGC ATC 2154 6631 2167 L S P R I N E E A G D T E CTC AGC CCC AGG ATA AAC GAA GAG GCT GGG GAC ACT GAG 6670 R T Q S A L A L S R A R S AGG ACC CAG TCG GCA TTG GCA CTG AGC AGA GCC CGG TCC 2180 6709 2193 ACC AAT GTC CAC AGC AAG ACC TCA GGA GAC AAG CCT GTT 6748 2206 K Y Η F R R S P Η F V

FIG. 2J

TCT CCC CAC TTT GTC CGC CGG CAA AAG TAC TGT CAT TTT G D G E V L A V Q R K S T GGG GAC GGC GAA GTG CTT GCC GTC CAG AGA AAG TCC ACA S T N T S P L S R E K L P AGT ACA AAT ACA TCC CCG CTG TCG AGG GAA AAG CTG CCC S P S A A L S E F V E G L AGT CCT TCA GCG GCC CTC TCG GAG TTC GTG GAA GGG CTC R R K R A Q R G Q G S T L CGG AGG AAG AGA GCC CAG AGA GGC CAG GGG TCC ACG CTG G L E D W P T L P I Y Q T GGC CTA GAG GAC TGG CCC ACT CTC CCC ATT TAC CAG ACG T G A S T L R R G R A G S ACT GGG GCC TCC ACA CTA AGG AGG GGC AGG GCT GGC AGT D E G N L S L R V G A K S GAC GAG GGA AAC CTC TCG CTG AGG GTT GGG GCA AAG TCA P L E I E G A A G G L L R CCC CTG GAA ATC GAA GGG GCC GCT GGT GGT CTC TTG AGG S T S L K C I S S D G V G TCC ACC AGC CTC AAA TGC ATC TCT TCA GAC GGT GTT GGG G T T L L P E K S K T Q F GGC ACA ACC CTA CTC CCC GAA AAG TCG AAA ACC CAA TTC S S C E S L L E S R P S M AGT TCC TGC GAG TCC CTC TTA GAA TCC AGA CCG AGC ATG  $\tt G$  R K L S S P T T P R D M GGG AGA AAA CTG AGC TCT CCG ACC ACA CCC AGG GAC ATG L L S P T L R P R R R C L CTG TTG TCG CCC ACA CTG CGT CCT CGG AGG CGG TGT CTG K E P L V F Q N R Q F A H AAG GAG CCG CTT GTT TTC CAG AAC CGC CAG TTT GCC CAC 

FIG. 2K

K	L	P	S	L	D	Y	E	R	K	T	K	V	2440
AAA	CTC	CCA	AGC	CTC	GAC	TAC	GAA	CGC	AAG	ACC	AAA	GTG	7489
D	F	D	D	F	L	P	A	I	R	K	P	Q	2453
GAC	TTC	GAT	GAC	TTC	CTC	CCA	GCT	ATC	CGG	AAG	CCC	CAG	7528
T	P	T	S	L	A	G	S	A	K	G	G	Q	2466
ACA	CCT	ACC	TCC	TTG	GCT	GGA	TCA	GCC	AAA	GGT	GGG	CAA	7567
D	G	S	Q	R	S	S	I	H	F	E	T	E	2479
GAC	GGT	TCA	CAG	CGT	TCA	AGC	ATC	CAC	TTT	GAA	ACG	GAA	7606
E	A	N	R	S	F	L	S	G	I	K	T	I	2492
GAG	GCT	AAC	CGT	TCC	TTT	CTC	TCG	GGG	ATC	AAG	ACC	ATT	7645
L	K	K	S	P	E	P	K	E	D	P	A	H	2505
TTG	AAG	AAG	AGC	CCG	GAG	CCC	AAG	GAG	GAT	CCC	GCT	CAC	7684
L	S	D	S	S	S	S	S	G	S	I	V	S	2518
CTG	TCT	GAC	TCG	TCC	TCA	TCC	TCC	GGC	TCC	ATC	GTG	TCC	7723
F	K	S	A	D	S	I	K	S	R	P	G	I	2531
TTC	AAA	AGT	GCT	GAC	AGC	ATC	AAA	AGT	CGA	CCA	GGA	ATC	7762
P	R	L	A	G	D	G	G	E	R	T	S	P	2544
CCA	CGA	CTT	GCG	GGT	GAC	GGT	GGC	GAG	CGA	ACG	TCC	CCC	7801
E	R	R	E	P	G	T	G	R	K	D	D	D	2557
GAG	CGG	AGA	GAG	CCA	GGG	ACG	GGG	AGG	AAA	GAC	GAC	GAT	7840
V GTT	A GCG	S AGC	I ATA	M ATG	K AAG	K AAA	Y TAC	L CTC	Q CAG	K AAG		gaa	2569 7879
cca	gttc	agcc	tcct	tgaa	gctg	ccct	tgaa	gact	tccc	gact	ctac	aataa	7931
cttggagacagagactggccaggcctccccggtggccagagccagcc								7983					
atggccaccctcaagaggcgagatgagcccacagaggcatatcctgcgggga								8035					
tgctgggctcccagtgtggttggcctgaacaaaataaagtgttgactcctgg									8087				
gcaaaaaaaaaaaaaaaaaaaaaa										8117			

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HGDMLP-1 BAA93660 BAA13206	APEDRWYEAEKVWLAOKDGFTLATVLKPDEGTADLPAGRVRLCIDADKTITEVDEEHVHR AAEEAWYETEKVWLVHRDGFSLASQLKSEELSLPEGKARVKLDHDGAILDVDEDDIEK	60 58
HGDMLP-1 BAA93660 BAA13206	ANPPELDQVEDLASLISVNESSVLNTLLQRYKAQLLHTCTGPDLIVLQPRGPSVPS ANAPSCDRLEDLASLVYLNESSVLHTLRQRYGASLLHTYAGPSLLVLSTRGAPAVYSEKV	116 118
HGDMLP-1 BAA93660 BAA13206	AGKVPKGRRDGLPAHIGSMAQRAYWALLNORRDOSIVALGRSGAGKTTCCEQVLEHLVGM MHMFKGCRREDMAPHIYAVAÕTAYRAMLMSRODÕSIVLLGSSGSGKTTSFOHLVQYLATI MHMFKGCRREDMAPHIYAVAÕTAYRAMLMSRÕDÕSIILLGSSGSGKTTSCÕHLVQYLATI . **::** ::** ** *:****: ** **:**** :::::::* :	178
HGDMLP-1 BAA93660 BAA13206	AGSVDGRVS-VEKIRATFTVLRAFGSVSMAHSRSATRFSMVMSLDFNATGRITAAOLOTM AGTSGTKVFSVEKWOALSTLLEAFGNSPTIMNGSATRFSQILSLDFDQAGQVASASIQTM AGISGNKVFSVEKWQALYTLLEAFGNSPTIINGNATRFSQILSLDFDQAGQVASASIQTM ** :* *** :* *:* *:* ***** :: **** :* :* :: ***	238
HGDMLP-1 BAA93660 BAA13206	LLEKSRVAROPEGESNFLVFSOMLAGLDLDLRTELNLHOMADSSSFGMGVWSKPEDKOKA LLEKLRVARRPASEATFNVFYYLLACGDATLRTELHLNHLAENNVFGIVPLSKPEEKOKA LLEKLRVARRPASEATFNVFYYLLACGDGTLRTELHLNHLAENNVFGIVPLAKPEEKOKA **** ***: *: *: ** ** ****************	298
HGDMLP-1 BAA93660 BAA13206	AAAFAOLOGAMEMLGISESEORAVWRVLAAIYHLGAAGACKVGRKOFMRFEWANYA AOOFSKLÕAAMKVLAISPEEÕKTCWLILASIYHLGAAGATKEAAEAGRKÕFARHEWAOKA AÕÕFSKLÕAAMKVLGISPDEÕKACWFILAAIYHLGAAGATKEAAEAGRKÕFARHEWAÕKA * *::**.**: * : * : * : * : * : * : * :	351 358 240
HGDMLP-1 BAA93660 BAA13206	AEALGCEYEELNTATFKHHLRQIIQOMTFGPSRWGLEDEETSSGLKMTGVDCVEGMAS AYLLGCSLEELSSAIFKHOLKGGTLÕRSTS-FROGPEESGLGEGTKLSALECLEGMAS AYLLGCSLEELSSAIFKHÕHKGGTLÕRSTS-FRÕGPEESGLGDGTGPKLSALECLEGMAA * *** ***: * ***: * * * * * * * * * * *	415
HGDMLP-1 BAA93660 BAA13206	GLYOELFAAVVSLINRSFSSHHLSMASIMVVDSPGFONPRHOGKDRAATFEELCHNYAHE GLYSELFTLLISLVNRALKSSOHSLCSMMIVDTPGFONPEWGGSARGASFEELCHNYAQD GLYSELFTLLVSLVNRALKSSOHSLCSMMIVDTPGFONPEQGGSARGASFEELCHNYTOD ***.**:::**:**:*:::*::::::::::::::::::	469 475 359
HGDMLP-1 BAA93660 BAA13206	RLOLLFYORTFVSTLORYOEEGVPVOFDLPDPSPGTTVAVVDONPSOOVRLPAGGGAQDA RLORLFHERTFLOELERYKEDNIELAFDDLEPVADDSVAAVDO-ASHLVRSLAHADEA RLORLFHERTFVOELERYKEENIELAFDDLEPPTDDSVAAVDO-ASHOSLVRSLARTDEA *** **::***: *:**:::::::::::::::::::::	532 418
HGDMLP-1 BAA93660 BAA13206	RGLFWVLDEEVHVEGSSDSVVLERLCATFEKKGAGTEGSSALRTCEOPLOCEIFHOLGWD RGLLWLLEEEALVPGATEDALLDRLFSYYGPOEGDKKGOSPLLRSSKPRHFLLGHSHGTN RGLLWLLEEEALVPGASEDTLLERLFSYYGPOEGDKKGOSPLLHSSKPHHFLLGHSHGTN ***:*:*:*: * * *:::::*:*: : : : : : * : * : : : * : * : : * : * : : : * : * : : * : * : : : * : * : : : * : : * : : : * : : : : * : : : : * : : : : * : : : : : * :	592
HGDMLP-1 BAA93660 BAA13206	PVRYDLTGWLHRAKPNLSALDAPOVLOOSKREELRSLFOARAKLPPVCR-AVAGLEGTSO WVEYNVAGWLNYTKONPATONAPRILODSOKKIISNLFIGRAGSATVLSGSIAGLEGGSO WVEYNVTGWLNYTKONPATONVPRLLODSOKKIISNLFLGRAGSATVLSGSIAGLEGGSO *.*:::***::* * :: : : *::**:* : : . * * . * .	652
HGDMLP-1 BAA93660 BAA13206	OALORSRMVRRTFASSLAAVRRKAPCSOIKLOMDALTSMIKRSRLHFIHCLVPNPVV LALRRATSMRKTFTTGMAAVKKKSLCIQIKLÖVDALIDTIKRSKMHFVHCFLPVAEGWPG LALRRATSMRKTFTTGMVAVKKKSLCIQMKLÖVDALIDTIKKSKLHFVHCFLPVAEGWAG **:*: :*:**::*:	/12

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HGDMLP-1 BAA93660 BAA13206	DOMOCODITITION OF BUILD TIME OF THE PROPERTY O	761 772 658
HGDMLP-1 BAA93660 BAA13206	ALOUI IGGG DANIE HULIGGIGGILLA ADDIGGIA DELLE DE	821 832 718
HGDMLP-1 BAA93660 BAA13206	ISRLEKOREKLVSQSIVLFQAACKGFLSROEFKKLKIRRLAAQCIQKNVAVFLAVKDWPW LARLEEÖRDEQTSRHLTLFÕAACRGYLARÕHFKKRKIQDLAIRCVÕKNIKKNKGVKDWPW LARLEEÖRDEQTSRNLTLFÕAACRGYLARÕHFKKRKIÕDLAIRCVÕKNIKKNKGVKDWPW ::***:**:	881 892 778
HGDMLP-1 BAA93660 BAA13206	WOLLGSLOPLLSATIGTEOLRAKEEELTTLRRKLEKSEKLRNELRONTDLLESKIADLTS WKLFTTVRPLIOVOLSEEOIRNKDEEIOOLRSKLEKVEKERNELRISSDRLETRISELTS WKLFTTVRPLIEVOLSEEOIRNKDEEIOOLRSKLEKAEKERNELRINSDRLESRISELTS *:*::::**: :: **: *:*:*:**: ** ***** :: **::***	941 952 838
HGDMLP-1 BAA93660 BAA13206	DLADERFKGDVACOVLESERAERLOAFREVOELKSKHEQVOKKLGDVNKQLEEAQOKIQL ELTDERNTGESASÕLLDAETAERLRTEKEMKELOTOYDALKKOMEVMEMEVMEARLIRAA ELTDERNTGESASÕLLDAETAERLRAEKEMKELÕTÕYDALKKOMEVMEMEVMEARLIRAA :*:***	1012
HGDMLP-1 BAA93660 BAA13206	N-DLERDPTGGADEWOMRFDCAQMENEFLRKRLQQ-CEERLDSELTARKELEQKLGELQS EINGEVDDDDAGGEWRLKYERAVREVDFTKKRLQQELEDKMEVEQQSRRQLERRLGDLQA EINGEVDDDDAGGEWRLKYERAVREVDFTKKRLQQEFEDKLEVEQQNKRQLERRLGDLQA :: * * **:::: * * :******* *::: * :::**::**	1072
HGDMLP-1 BAA93660 BAA13206	AYDGAKKMAHOLKRKCHHLTCDLEDTCVLLENOOSRNHELEKKOKKFDLOLAOALGESVF DSDESORALOOLKKKCORLTAELODTKLHLEGOOVRNHELEKKORRFDSELSOAHEETOR DSEESORALOOLKKKCORLTAELODTKLHLEGOOVRNHELEKKORRFDSELSOAHEEAOR : ::: :***:**:**:**:**:**:**:**:**:**:**	1132
HGDMLP-1 BAA93660 BAA13206	EKGLREKVTOENTSVRWELGOLOOOLKOKEQEASOLKOOVEMLODHKRELLGSPSLGENC EKLOREKLOREKDMLLAEAFSLKÕÕMEEKDLDIAGFTOKVVSLEAELODISSOESKDEAS EKLÕREKLÕREKDMLLAEAFSLKÕÕLEEKDMDIAGFTOKVVSLEAELÕDISSÕESKDEAS ** ***: : * : * : * : * : * : * : : : :	1192
HGDMLP-1 BAA93660 BAA13206	VAGLKERLWKLESSALEOOKIOSOOENTIKOLEOLRORFELEIERMKOMHOKDREDOEEE LAKVKKOLRDLEAKVKDÕEEELDEÕAGSIOMLEÕAKLRLEMEMERMRÕTHŠKEMESRDEE LAKVKKOLRDLEAKVKDÕEEELDEÕAGTIOMLEÕAKLRLEMEMERMRÕTHSKEMESRDEE :*:*:*:*:*:*:*:*:*:*:	1252
HGDMLP-1 BAA93660 BAA13206	LEDVROSCOKRLHOLEMOLEOEYEEKOMVLHEKODLEGLIGTLCDOIGHRDFDVEKRLRR VEEAROSCOKKLKOMEVOLEEEYEDKOKALREKRELESKLSTLSDOVNORDFESEKRLRK VEEAROSCOKKLKOMEVOLEEEYEDKOKVLREKRELEGKLATLSDOVNRRDFESEKRLRK :*:.*****::*:*:**:**:**:	1312
HGDMLP-1 BAA93660 BAA13206	DLRRTHALLSDVOLLLGTMEDGKTSVSKEELEKVHSQLEQSEAKCEEALKTOKVLTADLE DLKRTKALLADAÕIMLDHLKNNAPSKREIAQLKNÕLEESEFTCAAAVKARKAMEVEME DLKRTKALLADAÕLMLDHLKNSAPSKREIAQLKNÕLEESEFTCAAAVKARKAMEVEIE **:**:**:*::*:::::::::::::::::::::::	1370
HGDMLP-1 BAA93660 BAA13206	SMHSELENMTRNKSLVDEOLYRLOFEKADLLKRIDEDODDLNELMOKHKDLIAOSAADIG DLHLOIDDIAKAKTALEEÖLSRLÖREKNEIONRLEEDOEDMNELMKKHKAAVAOASRDMA DLHLQIDDIAKAKTALEEOLSRLÖREKNEIONRLEEDOEDMNELMKKHKAAVAOASRDLA	1430

HGDMLP-1 BAA93660 BAA13206		1479 1490 1376
HGDMLP-1 BAA93660 BAA13206	KTÖVKRLENLASRLKETMEKLTEERDÕRAAAENŘĚKEONŘRLÕROLRDTKEEMSELAŘKE	1539 1550 1436
HGDMLP-1 BAA93660 BAA13206	AEASRKKHELEMDLESLEAANÕSLÕADLKLAFKRIGDLÕAAIEDEMESDENEDLIÑSEGD	1599 1610 1496
HGDMLP-1 BAA93660 BAA13206	CGSSGRKEMDNVSILSSQPEGSLQSWLSCTLSLATDTMRTPSRQSATSSRILSPRINEEA SKNKGPSK SDVDSELEDRVDG-VKSWLSKNKGPSK * * * : * : : * * : * * * * . : * * : * * : * * * . : * * : * * * *	1659 1636 1522
HGDMLP-1 BAA93660 BAA13206	GDTERTQSALALSRARSTNVHSKTSGDKPVSPHFVRRQKYCHFGDGEVLAVQRKSTERLEAPSDDGSLKSSSPTSHWKPLAPDPSDDEHDPVDAASDDGSLKSSSPTSYWKSLAPDRSDDEHDPLD * * * : * * * .:: * . : : : : : : : : :	1719 1669 1555
HGDMLP-1 BAA93660 BAA13206	PASSPLASRSTNTSPLSREKLPSPSA 1745 SISRPRFSHSYLSDSDTEAKLTETSA 1695 NTSRPRYSHSYLSDSDTEAKLTETNA 1581 * * *:* : : . ***	

FIG. 3C

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### Sequences Aligned

Query: myocilin (Homo sapiens): Length 504 (1 .. 504)

Sbjct: hGDMLP-1: Length 2568 (1 .. 2568)

#### Region of Optimal Alignment

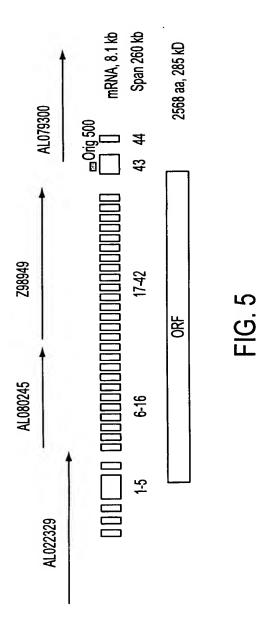
RLDLEATKARLSSLESLLHQLTLDQAARPQETQEGLQRELGTLRRERDQ-LETQ---TRE 137 Query: 82 R DL T A LS ++ LL + + + + E E + + L + + + L+TQ T + Sbjct: 1802 RRDLRTHALLSDVQLLLGTMEDGKTSVSKEELEKVHSQLEQSEAKCEEALKTQKVLTAD 1861

Query: 138 LETAYS---NLLRDKSVLEEEKKRLRQENENLARRLESSSQEVARL 180 LE+ +S N+ R+KS+++E+ RL+ E +L +R++ ++ L Sbjct: 1862 LESMHSELENMTRNKSLVDEQLYRLQFEKADLLKRIDEDQDDLNEL 1907

#### **Statistics**

Identities = 30/106 (28%), Positives = 58/106 (54%), Gaps = 7/106 (6%)

FIG. 4



# BEST AVAILABLE COPY

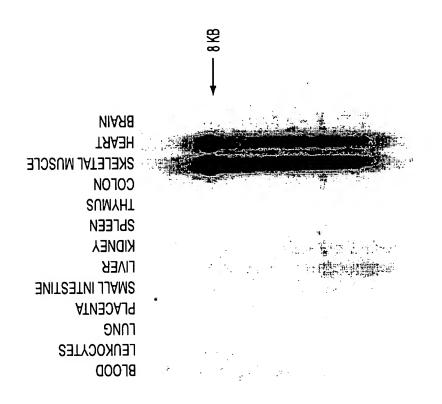


FIG. 6